OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/083,720A**

DATE: 07/24/2002
TIME: 11:33:44

Input Set : **A:\Seq listing DX0644KBK.ST25.txt**
Output Set: **N:\CRF3\07242002\J083720A.raw**

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  3  <110> APPLICANT: de Waal Malefyt, Rene
  4          Fickenscher, Helmut
  5          Fleckenstein, Bernhard
  6          Knappe, Andrea
  8  <120> TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
 10  <130> FILE REFERENCE: DX0644KBK
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C--> 12 **<140> CURRENT APPLICATION NUMBER: US/10/083,720A**
C--> 12 **<141> CURRENT FILING DATE: 2002-02-28**
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 12  <150> PRIOR APPLICATION NUMBER: 09/363,993
 13  <151> PRIOR FILING DATE: 1999-07-29
 15  <150> PRIOR APPLICATION NUMBER: 08/934,959
 16  <151> PRIOR FILING DATE: 1997-09-22
 18  <150> PRIOR APPLICATION NUMBER: 60/345,690
 19  <151> PRIOR FILING DATE: 2002-01-03
 21  <150> PRIOR APPLICATION NUMBER: 60/302,176
 22  <151> PRIOR FILING DATE: 2001-06-28
 24  <150> PRIOR APPLICATION NUMBER: 60/027,368
 25  <151> PRIOR FILING DATE: 1996-09-23
 27  <160> NUMBER OF SEQ ID NOS: 21
 29  <170> SOFTWARE: PatentIn version 3.1
 31  <210> SEQ ID NO: 1
 32  <211> LENGTH: 1076
 33  <212> TYPE: DNA
 44  <213> ORGANISM: Homo sapiens
 46  <220> FEATURE:
 47  <221> NAME/KEY: CDS
 48  <222> LOCATION: (36)..(548)
 49  <223> OTHER INFORMATION:
 42  <400> SEQUENCE: 1
 43  ctgtgagtga cacacgctga gtggggtgaa gggaa atg ctg gtg aat ttc att        53
 44                                        Met Leu Val Asn Phe Ile
 45                                         1               5
 47  ttg agg tgt ggg ttg ctg tta gtc act ctg tct ctt gcc att gcc aag      101
 48  Leu Arg Cys Gly Leu Leu Leu Val Thr Leu Ser Leu Ala Ile Ala Lys
 49          10               15                  20
```

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61 55                    60                65                    70
63 aca aaa aag cag ttt atg aaa aac tgt caa ttt caa gaa cag ctt ctg    293
64 Thr Lys Lys Gln Phe Met Lys Asn Cys Gln Phe Gln Glu Gln Leu Leu
65                    75                80                    85
67 tcc ttc ttc atg gaa gac gtt ttt ggt caa ctg caa ttg caa ggc tgc    341
68 Ser Phe Phe Met Glu Asp Val Phe Gly Gln Leu Gln Leu Gln Gly Cys
69                    90                95                    100
71 aag aaa ata cgc ttt gtg gag gac ttt cat agc ctt agg cag aaa ttg    389
72 Lys Lys Ile Arg Phe Val Glu Asp Phe His Ser Leu Arg Gln Lys Leu
73          105                110                115
75 agc cac tgt att tcc tgt gct tca tca gct aga gag atg aaa tcc att    437
76 Ser His Cys Ile Ser Cys Ala Ser Ser Ala Arg Glu Met Lys Ser Ile
77      120                125                130
79 acc agg atg aaa aga ata ttt tat agg att gga aac aaa gga atc tac    485
80 Thr Arg Met Lys Arg Ile Phe Tyr Arg Ile Gly Asn Lys Gly Ile Tyr
81 135                140                145                    150
83 aaa gcc atc agt gaa ctg gat att ctt ctt tcc tgg att aaa aaa tta    533
84 Lys Ala Ile Ser Glu Leu Asp Ile Leu Leu Ser Trp Ile Lys Lys Leu
85                    155                160                    165
87 ttg gaa agc agt cag taaaccaaag ccaagtacat tgattttaca gttattttga    588
88 Leu Glu Ser Ser Gln
89                170
91 aatacaataa gaactgctag aaatatgttt ataacagtct atttctttta aaaacttttt    648
93 aacataaatac tgacggcatg ttaggtgatt cagaatagac aagaaggatt tagtaaatta    708
95 acgttttgga tataagttgt cactaatttg cacattttct gtgttttcaa ataatgtttc    768
97 cattctgaac atgtttttgtc attcacaagt acattgtgtc aacttaattt aaagtatgta    828
99 acctgaatta actcgtgtaa tatttgtgtg tggagtggga tgtgggggt ggaggggaa    888
101 tgacagattt ctggaatgca atgtaatgtt actgagactt aaatagatgt tatgtatatg    948
103 attgtctgtt taagtgtttg aaaattgtta attatgccca gtgtgaactt agtacttaac   1008
105 acattttgat tttaattaaa taaattgggt ttccttctca aaaaaaaaaa aaaaaaaaaa   1068
107 aaaaaaaa                                                            1076
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 171
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
117 Met Leu Val Asn Phe Ile Leu Arg Cys Gly Leu Leu Leu Val Thr Leu
118 1                5                10                    15
121 Ser Leu Ala Ile Ala Lys His Lys Gln Ser Ser Phe Thr Lys Ser Cys
122          20                25                30
125 Tyr Pro Arg Gly Thr Leu Ser Gln Ala Val Asp Ala Leu Tyr Ile Lys
126      35                40                45
129 Ala Ala Trp Leu Lys Ala Thr Ile Pro Glu Asp Arg Ile Lys Asn Ile
130      50                55                60
```

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```
142               100              105              110
145 Ser Leu Arg Gln Lys Leu Ser His Cys Ile Ser Cys Ala Ser Ser Ala
146       115              120              125
149 Arg Glu Met Lys Ser Ile Thr Arg Met Lys Arg Ile Phe Tyr Arg Ile
150     130              135              140
153 Gly Asn Lys Gly Ile Tyr Lys Ala Ile Ser Glu Leu Asp Ile Leu Leu
154 145              150              155              160
157 Ser Trp Ile Lys Lys Leu Leu Glu Ser Ser Gln
158               165              170
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 179
163 <212> TYPE: PRT
164 <213> ORGANISM: Equine Herpes Virus
166 <400> SEQUENCE: 3
168 Met Phe Arg Ala Ser Leu Leu Cys Cys Leu Val Leu Leu Ala Gly Val
169 1               5                10               15
172 Trp Ala Asp Asn Lys Tyr Asp Ser Glu Ser Gly Asp Asp Cys Pro Thr
173               20               25               30
176 Leu Pro Thr Ser Leu Pro His Met Leu His Glu Leu Arg Ala Ala Phe
177       35               40               45
180 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Met
181     50               55               60
184 Leu Leu Asp Gly Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
185 65               70               75               80
188 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
189               85               90               95
192 Gln Ala Glu Asn His Ser Thr Asp Gln Glu Lys Asp Lys Val Asn Ser
193               100              105              110
196 Leu Gly Glu Lys Leu Lys Thr Leu Arg Val Arg Leu Arg Arg Cys His
197       115              120              125
200 Arg Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys
201     130              135              140
204 Ser Ala Phe Ser Lys Leu Gln Glu Lys Gly Val Tyr Lys Ala Met Ser
205 145              150              155              160
208 Glu Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Thr Lys
209              165              170              175
212 Met Lys Asn
216 <210> SEQ ID NO: 4
217 <211> LENGTH: 170
218 <212> TYPE: PRT
219 <213> ORGANISM: Epstein Barr Virus
221 <400> SEQUENCE: 4
223 Met Glu Arg Arg Leu Val Val Thr Leu Gln Cys Leu Val Leu Leu Tyr
224 1               5                10               15
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Input Set : **A:\Seq listing DX0644KBK.ST25.txt**
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```
236       50                    55                   60
239 Glu Asp Phe Lys Gly Tyr Leu Gly Cys Gln Ala Leu Ser Glu Met Ile
240 65                    70                   75                   80
243 Gln Phe Tyr Leu Glu Glu Val Met Pro Gln Ala Glu Asn Gln Asp Pro
244               85                   90                   95
247 Glu Ala Lys Asp His Val Asn Ser Leu Gly Glu Asn Leu Lys Thr Leu
248               100                  105                  110
251 Arg Leu Arg Leu Arg Arg Cys His Arg Phe Leu Pro Cys Glu Asn Lys
252           115                  120                  125
255 Ser Lys Ala Val Glu Gln Ile Lys Asn Ala Phe Asn Lys Leu Gln Glu
256       130                  135                  140
259 Lys Gly Ile Tyr Lys Ala Met Ser Glu Phe Asp Ile Phe Ile Asn Tyr
260 145                  150                  155                  160
263 Ile Glu Ala Tyr Met Thr Ile Lys Ala Arg
264               165                  170
267 <210> SEQ ID NO: 5
268 <211> LENGTH: 178
269 <212> TYPE: PRT
270 <213> ORGANISM: Mus musculus
272 <400> SEQUENCE: 5
274 Met Pro Gly Ser Ala Leu Leu Cys Cys Leu Leu Leu Leu Thr Gly Met
275 1                 5                    10                   15
278 Arg Ile Ser Arg Gly Gln Tyr Ser Arg Glu Asp Asn Asn Cys Thr His
279           20                   25                   30
282 Phe Pro Val Gly Gln Ser His Met Leu Leu Glu Leu Arg Thr Ala Phe
283           35                   40                   45
286 Ser Gln Val Lys Thr Phe Phe Gln Thr Lys Asp Gln Leu Asp Asn Ile
287       50                   55                   60
290 Leu Leu Thr Asp Ser Leu Met Gln Asp Phe Lys Gly Tyr Leu Gly Cys
291 65                   70                   75                   80
294 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Val Glu Val Met Pro
295               85                   90                   95
298 Gln Ala Glu Lys His Gly Pro Glu Ile Lys Glu His Leu Asn Ser Leu
299               100                  105                  110
302 Gly Glu Lys Leu Lys Thr Leu Arg Met Arg Leu Arg Arg Cys His Arg
304           115                  120                  125
306 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Ser
307       130                  135                  140
310 Asp Phe Asn Lys Leu Gln Asp Gln Gly Val Tyr Lys Ala Met Asn Glu
311 145                  150                  155                  160
314 Phe Asp Ile Phe Ile Asn Cys Ile Glu Ala Tyr Met Met Ile Lys Met
315               165                  170                  175
318 Lys Ser
322 <210> SEQ ID NO: 6
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```
330 1                   5                   10                  15
333 Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
334                 20                  25                  30
337 Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
338             35                  40                  45
341 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
342         50                  55                  60
345 Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
346 65                  70                  75                  80
349 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
350                 85                  90                  95
353 Gln Ala Glu Asn Gln Asp Pro Asp Ile Lys Ala His Val Asn Ser Leu
354                 100                 105                 110
357 Gly Glu Asn Leu Lys Thr Leu Arg Leu Arg Leu Arg Arg Cys His Arg
358             115                 120                 125
361 Phe Leu Pro Cys Glu Asn Lys Ser Lys Ala Val Glu Gln Val Lys Asn
362         130                 135                 140
365 Ala Phe Asn Lys Leu Gln Glu Lys Gly Ile Tyr Lys Ala Met Ser Glu
366 145                 150                 155                 160
369 Phe Asp Ile Phe Ile Asn Tyr Ile Glu Ala Tyr Met Thr Met Lys Ile
370                 165                 170                 175
373 Arg Asn
377 <210> SEQ ID NO: 7
378 <211> LENGTH: 20
379 <212> TYPE: DNA
380 <213> ORGANISM: Artificial Sequence
382 <220> FEATURE:
383 <223> OTHER INFORMATION: IL-8 forward.
385 <220> FEATURE:
386 <221> NAME/KEY: misc_feature
387 <222> LOCATION: (1)..(20)
388 <223> OTHER INFORMATION: IL-8 forward probe
391 <400> SEQUENCE: 7
392 tggcagcctt cctgatttct                                         20
395 <210> SEQ ID NO: 8
396 <211> LENGTH: 26
397 <212> TYPE: DNA
398 <213> ORGANISM: Artificial Sequence
400 <220> FEATURE:
401 <223> OTHER INFORMATION: IL-8 reverse.
403 <220> FEATURE:
404 <221> NAME/KEY: misc_feature
405 <222> LOCATION: (1)..(26)
406 <223> OTHER INFORMATION: IL-8 reverse probe.
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VERIFICATION SUMMARY   DATE: 07/24/2002
PATENT APPLICATION: **US/10/083,720A**   TIME: 11:33:45

Input Set : **A:\Seq listing DX0644KBK.ST25.txt**
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date